In the Specification:

Please amend the specification as shown:

Please delete the paragraph on page 38, line 25 and replace it with the following paragraph:

-- Figure 7 shows the amino acid sequence of TSST-1 **(SEQ ID NO: 45)**; --

Please delete the paragraph on page 38, line 27-28 and replace it with the following paragraph:

-- Figure 9 shows aligned amino acid sequences of DSL domains from various Drosophila and mammalian Notch ligands **(SEQ ID NOS 24-39, respectively, in order of appearance)**; --

Please delete the paragraph on page 38, line 29 and replace it with the following paragraph:

-- Figure 10 shows amino acid sequences of human Delta-1 **(SEQ ID NO: 40)**, Delta-3 **(SEQ ID NO: 41)** and Delta-4 **(SEQ ID NO: 42)**; and --

Please delete the paragraph on page 38, line 30 and replace it with the following paragraph:

-- Figure 11 shows amino acid sequences of human Jagged-1 **(SEQ ID NO: 43)** and Jagged-2 **(SEQ ID NO: 44)**. --

Please delete the paragraph on page 50, lines 42-47 and replace it with the following paragraph:

-- A typical DSL domain may include most or all of the following consensus amino acid sequence:

```
Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa
Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys (SEQ ID NO: 1) --
```

Please delete the paragraph on page 50, lines 49-54 and replace it with the following paragraph:

-- Preferably the DSL domain may include most or all of the following consensus amino acid sequence:

Cys Xaa Xaa Xaa ARO ARO Xaa Xaa Xaa Cys Xaa Xaa Xaa Cys BAS NOP
BAS ACM ACM Xaa ARO NOP ARO Xaa Xaa Cys Xaa Xaa Xaa NOP Xaa Xaa
Xaa Cys Xaa Xaa NOP ARO Xaa NOP Xaa Xaa Cys **(SEQ ID NO: 2)** --

Please delete the paragraph on page 51, lines 15-22 and replace it with the following paragraph:

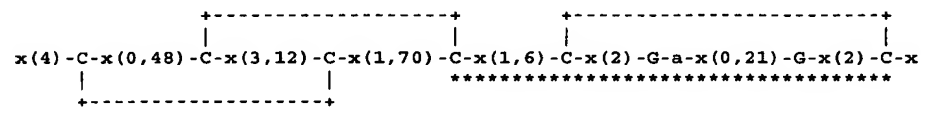
-- Preferably the DSL domain may include most or all of the following consensus amino acid sequence:

Cys Xaa Xaa Xaa Tyr Tyr Xaa Xaa Xaa Cys Xaa Xaa Xaa Cys Arg Pro
Arg Asx Asp Xaa Phe Gly His Xaa Xaa Cys Xaa Xaa Xaa Gly Xaa Xaa
Xaa Cys Xaa Xaa Gly Trp Xaa Gly Xaa Xaa Cys **(SEQ ID NO: 3)**

(wherein Xaa may be any amino acid and Asx is either aspartic acid or asparagine). --

Please delete the paragraph on page 53, lines 1-21 and replace it with the following paragraph:

-- As reported by PROSITE the EGF domain typically includes six cysteine residues which have been shown (in EGF) to be involved in disulfide bonds. The main structure is proposed, but not necessarily required, to be a two-stranded beta-sheet followed by a loop to a C-terminal short two-stranded sheet. Subdomains between the conserved cysteines strongly vary in length as shown in the following schematic representation of the EGF-like domain **(SEQ ID NO: 4)**:



wherein:

'C': conserved cysteine involved in a disulfide bond.

'G': often conserved glycine

'a': often conserved aromatic amino acid

'*': position of both patterns.

'x': any residue --

Please delete the paragraph on page 66, lines 16-35 and replace it with the following paragraph:

-- A fragment of human Jagged 1 (hJag1) cDNA (see for example GenBank Accession No U61276) coding for the sequence from amino acid 1 of the immature protein sequence (i.e. the Met (M) residue used to initiate transcription) through to amino acid 296 (Asp (D)) was prepared in a pcDNA3.1 expression vector (Invitrogen, Carlsbad, CA, USA and Paisley, UK). The nucleic acid sequence of the Jagged 1 cDNA fragment was as follows:

atgcgttccccacggacgcgcggccggtccgggcgccccctaagcctcctgctcgccctgctctgtgccctgcga
gccaaggtgtgtggggcctcgggtcagttcgagttggagatcctgtccatgcagaacgtgaacggggagctgcag
aacgggaactgctgcggcggcgcccggaacccgggagaccgcaagtgcacccgcgacgagtgtgacacatacttc
aaagtgtgcctcaaggagtatcagtcccgcgtcacggccgggggccctgcagcttcggctcagggtccacgcct
gtcatcgggggcaacaccttcaacctcaaggccagccgcggcaacgaccgcaaccgcatgctgcctttcagtttc
gcctggccgaggtcctatacgttgcttgtggaggcgtgggattccagtaatgacaccgttcaacctgacagtatt
attgaaaaggcttctcactcgggcatgatcaaccccagccggcagtggcagacgctgaagcagaacacgggcgtt
gcccactttgagtatcagatccgcgtgacctgtgatgactactactatggctttggctgcaataagttctgccgc
cccagagatgacttctttggacactatgcctgtgaccagaatggcaacaaaacttgcatggaaggctggatgggc
cccgaatgtaacagagctatttgccgacaaggctgcagtcctaagcatgggtcttgcaaactcccaggtgactgc
aggtgccagtatggctggcaaggcctgtactgtgataagtgcatcccacacccgggatgcgtccacggcatctgt
aatgagccctggcagtgcctctgtgagaccaactggggcggccagctctgtgacaa***agatct***
(SEQ ID NO: 5) --

Please delete the paragraph on page 67, lines 4-5 and replace it with the following paragraph:

-- hJag1 amino acids 1-296; $(Gly\text{-}Ser)_5$ artificial linker **(SEQ ID NO: 8)**; TSST-1 N-terminal sequence amino acids 1-90.

Please delete the paragraph on page 67, lines 8-14 and replace it with the following paragraph:

-- The hJag1 296 amino acid fragment in the resulting fusion protein had the following amino acid sequence **(SEQ ID NO: 6)**:

```
  1  MRSPRTRGRS GRPLSLLLAL LCALRAKVCG ASGQFELEIL SMQNVNGELQ NGNCCGGARN
 61  PGDRKCTRDE CDTYFKVCLK EYQSRVTAGG PCSFGSGSTP VIGGNTFNLK ASRGNDPNRI
121  VLPFSFAWPR SYTLLVEAWD SSNDTVQPDS IIEKASHSGM INPSRQWQTL KQNTGVAHFE
181  YQIRVTCDDY YYGFGCNKFC RPRDDFFGHY ACDQNGNKTC MEGWMGPECN RAICRQGCSP
241  KHGSCKLPGD CRCQYGWQGL YCDKCIPHPG CVHGICNEPW QCLCETNWGG QLCDKD  --
```

Please delete the paragraph on page 67, lines 16-20 and replace it with the following paragraph:

-- The TSST-1 N-terminal 90 amino acid fragment in the resulting fusion protein had the following amino acid sequence **(SEQ ID NO: 7)**:

```
  1  STNDNIKDLL DWYSSGSDTF TNSEVLDNSL GSMRIKNTDG SISLIIFPSP YYSPAFTKGE
 61  KVDLNTKRTK KSQHTSEGTY IHFQISGVTN  --
```

Please delete the paragraph on page 67, lines 22-23 and replace it with the following paragraph:

-- The $(Gly\text{-}Ser)_5$ artificial linker sequence in the resulting fusion protein had the amino acid sequence: GSGSGSGSGS **(SEQ ID NO: 8)** --

Please delete the paragraph on page 67, lines 25-33 and replace it with the following paragraph:

-- To provide the TSST/linker portion of the fusion protein, a polynucleotide coding TSST-1 N-terminal sequence amino acids 1-90 and the 5' $(Gly\text{-}Ser)_5$ linker was generated with the following nucleic acid sequence:

gat ctc ggc tct ggt agc gga agt ggc agc ggc tct agt act aac gac aac atc aag gat ctg ctt gac tgg tac tct tcc ggg tcg gat aca ttt acg aat agc gaa gta tta gat aat tca cta ggc tca atg aga ata aaa aac acc gac ggc tcc ata agt ctc atc att ttt cca agt cca tat tat tcg cca gca ttc aca aaa ggt gaa aaa gta gat ttg aat aca aag aga act aaa aag tct caa cac acc agt gag gga acg tac ata cat ttc cag att agc gga gta aca aat tga (stop) **(SEQ ID NO: 9)** --

Please delete the paragraph on page 67, line 35 to page 68, line 19 and replace it with the following paragraph:

-- This polynucleotide was generated by gene assembly (using oligonucleotide primers followed by PCR amplification using oligonucleotide primers designed to amplify from the 5' and 3' ends at the same time as introducing BglII and EcoRI sites respectively), by annealing overlapping "upper strand" and "lower strand" primers (selected such that the upper and lower strand primers overlap with each other by approximately 12-15 base pairs) as follows:

upper strand primers: Gm40, 42, 44, 46 and 48:

Gm40: ata aga atc aga tct cgg ctc tgg tag cgg aag tgg cag cgg ctc tag tac t
(SEQ ID NO: 10)
Gm42: gat ctg ctt gac tgg tac tct tcc ggg tcg gat aca ttt acg aat agc
(SEQ ID NO: 11)
Gm44: ggc tca atg aga ata aaa aac acc gac ggc tcc ata agt ctc atc att ttt
(SEQ ID NO: 12)
Gm46: gca ttc aca aaa ggt gaa aaa gta gat ttg aat aca aag aga act aaa aag
(SEQ ID NO: 13)
Gm48: acg tac ata cat ttc cag att agc gga gta aca aat tga gaa ttc ata aga atg
(SEQ ID NO: 14)

lower strand primers: Gm41, 43, 45, 47 and 50:

Gm41: cca gtc aag cag atc ctt gat gtt gtc gtt agt act aga gcc gct gcc act
(SEQ ID NO: 15)
Gm43: tat tct cat tga gcc tag tga att atc taa tac ttc gct att cgt aaa tgt
(SEQ ID NO: 16)
Gm45: acc ttt tgt gaa tgc tgg cga ata ata tgg act tgg aaa aat gat gag act tat
(SEQ ID NO: 17)
Gm47: gaa atg tat gta cgt tcc ctc act ggt gtg ttg aga ctt ttt agt tct ctt tgt
(SEQ ID NO: 18)
Gm50: cat tct tat gaa ttc tc
(SEQ ID NO: 19) --

Please delete the paragraph on page 69, line 27 to page 70, line 2 and replace it with the following paragraph:

-- An adenovirus major late promoter TATA-box motif with BglII and HindIII cohesive ends was generated as follows:

BglII HindIII

GATCTGGGGGGCTATAAAAGGGGGTA (SEQ ID NO: 20)

ACCCCCCGATATTTTCCCCCATTCGA (SEQ ID NO: 21)

This was cloned into plasmid pGL3-Basic (Promega) between the BglII and HindIII sites to generate plasmid pGL3-AdTATA. --

Please delete the paragraph on page 70, lines 4-9 and replace it with the following paragraph:

-- A TP1 promoter sequence (TP1; equivalent to 2 CBF1 repeats) with BamH1 and BglII cohesive ends was generated as follows:

BamH1 BglII

5' GATCCCGACTCGTGGGAAAATGGGCGGAAGGGCACCGTGGGAAAATAGTA 3' (SEQ ID NO: 22)

3' GGCTGAGCACCCTTTTACCCGCCTTCCCGTGGCACCCTTTTATCATCTAG 5'

(SEQ ID NO: 23) --